

FIG.1

Nucleotide sequence of ATCC21529 ask (SEQ ID NO:1)

```

1  GTGGCCCTGG TCGTACAGAA ATATGGCGGT TCCTCGCTTG AGAGTGCGGA
51  ACGCATTAGA AACGTCGCTG AACGGATCGT TGCCACCAAG AAGGCTGGAA
101 ATGATGTCGT GGTGTCTGC TCCGCAATGG GAGACACCAC GGATGAACTT
151 CTAGAACTTG CAGCGGCAGT GAATCCCGTT CCGCCAGCTC GTGAAATGGA
201 TATGCTCCTG ACTGCTGGTG AGCGTATTTC TAACGCTCTC GTCGCCATGG
251 CTATTGAGTC CTTGGCGCA GAAGCTCAAT CTTTCACTGG CTCTCAGGCT
301 GGTGTGCTCA CCACCGAGCG CCACGGAAAC GCACGCATTG TTGACGTCAC
351 ACCGGGTCGT GTGCGTGAAG CACTCGATGA GGGCAAGATC TGCATTGTTG
401 CTGGTTTTC AAGGTGTTAAT AAAGAAACCC GCGATGTCAC CACGTTGGGT
451 CGTGGTGGTT CTGACACCAC TGCAGTTGCG TTGGCAGCTG CTTTGAACGC
501 TGATGTGTGT GAGATTTACT CGGACGTTGA CGGTGTGTAT ACCGCTGACC
551 CGCGCATCGT TCCTAATGCA CAGAAGCTGG AAAAGCTCAG CTTCGAAGAA
601 ATGCTGGAAC TTGCTGCTGT TGGCTCCAAG ATTTTGGTGC TGCAGTGTG
651 TGAATACGCT CGTGCAATCA ATGTGCCACT TCGCGTACGC TCGTCTTATA
701 GTAATGATCC CGGCACTTTG ATTGCCGGCT CTATGGAGGA TATTCCTGTG
751 GAAGAAGCAG TCCTTACCGG TGTCGCAACC GACAAGTCCG AAGCCAAAGT
801 AACCGTTCTG GGTATTTCCG ATAAGCCAGG CGAGGCTGCC AAGGTTTTCC
851 GTGCGTTGGC TGATGCAGAA ATCAACATTG ACATGGTTCT GCAGAAcgtc
901 tcctctgtGG AAGACGGCAC CACCGACATC ACGTTCACCT GCCCTCGCGC
951 TGACGGACGC CGTGCGATGG AGATCTTGAA GAAGCTTCAG GTTCAGGGCA
1001 ACTGGACCAA TGTGCTTTAC GACGACCAGG TCGGCAAAGT CTCCCTCGTG
1051 GGTGCTGGCA TGAAGTCTCA CCCAGGTGTT ACCGCAGAGT TCATGGAAGC
1101 TCTGCGCGAT GTCAACGTGA ACATCGAATT GATTTCCATC TCTGAGATCC
1151 GCATTTCCGT GCTGATCCGT GAAGATGATC TGGATGCTGC TGCACGTGCA
1201 TTGCATGAGC AGTTCCAGCT GGGCGGCGAA GACGAAGCCG TCGTTTATGC
1251 AGGCACCGGA CGCTAA

```

FIG. 2

Amino Acid Sequence of ATTC21529 ask (SEQ ID NO:2)

```

1  GTGGCCCTGGTCGTACAGAAATATGGCGGTTCTCGCTTGAGAGTGCAGAACGCATTAGA 60
   M A L V V Q K Y G G S S L E S A E R I R
61  AACGTCGCTGAACGGATCGTTGCCACCAAGAAGGCTGGAAATGATGTCGTGGTTGTCTGC 120
   N V A E R I V A T K K A G N D V V V V C
121 TCCGCAATGGGAGACACCACGGATGAACCTTCTAGAACTTGCAGCGGCAGTGAATCCC GTT 180
   S A M G D T T D E L L E L A A A V N P V
   CCGCCAGCTCGTGAAATGGATATGCTCCTGACTGCTGGTGAGCGTATTTCTAACGCTCTC
181 -----+-----+-----+-----+-----+-----+ 240
   P P A R E M D M L L T A G E R I S N A L
   GTCGCCATGGCTATTGAGTCCCTTGGCGCAGAAGCTCAATCTTTCAGTGGCTCTCAGGCT
241 -----+-----+-----+-----+-----+-----+ 300
   V A M A I E S L G A E A Q S F T G S Q A
   GGTGTGCTCACCACCGAGCGCCACGAAACGCACGCATTGTTGACGTCACACCGGGTCGT
301 -----+-----+-----+-----+-----+-----+ 360
   G V L T T E R H G N A R I V D V T P G R
   GTGCGTGAAGCACTCGATGAGGGCAAGATCTGCATTGTTGCTGGTTTTAGGGTGTTAAT
361 -----+-----+-----+-----+-----+-----+ 420
   V R E A L D E G K I C I V A G F Q G V N
   AAAGAAACCCGCGATGTCACCACGTTGGGTCGTGGTGGTTCTGACACCACTGCAGTTGCG
421 -----+-----+-----+-----+-----+-----+ 480
   K E T R D V T T L G R G G S D T T A V A
   TTGGCAGCTGCTTTGAACGCTGATGTGTGTGAGATTTACTCGGACGTTGACGGTGTGTAT
481 -----+-----+-----+-----+-----+-----+ 540
   L A A A L N A D V C E I Y S D V D G V Y
   ACCGCTGACCCGCGCATCGTTCCTAATGCACAGAAGCTGGAAAAGCTCAGCTTCGAAGAA
541 -----+-----+-----+-----+-----+-----+ 600
   T A D P R I V P N A Q K L E K L S F E E
   ATGCTGGAACCTTGCTGCTGTTGGCTCCAAGATTTTGGTGCTGCGCAGTGTTGAATACGCT
601 -----+-----+-----+-----+-----+-----+ 660
   M L E L A A V G S K I L V L R S V E Y A

```

FIG.3A

```

661  CGTGCATTCAATGTGCCACTTCGCGTACGCTCGTCTTATAGTAATGATCCCGGCACTTTG 720
      -----+-----+-----+-----+-----+-----+
      R A F N V P L R V R S S Y S N D P G T L
841  ATTGCCGGCTCTATGGAGGATATTCCTGTGGAAGAAGCAGTCCTTACCGGTGTCGCAACC 900
      -----+-----+-----+-----+-----+-----+
      I A G S M E D I P V E E A V L T G V A T
841  GACAAGTCCGAAGCCAAAGTAACCGTTCTGGGTATTTCCGATAAGCCAGGCGAGGCTGCC 900
      -----+-----+-----+-----+-----+-----+
      D K S E A K V T V L G I S D K P G E A A
      AAGGTTTTCCGTGCGTTGGCTGATGCAGAAATCAACATTGACATGGTTCTGCAGAAcgtc
841  -----+-----+-----+-----+-----+-----+ 900
      K V F R A L A D A E I N I D M V L Q N V
      tcctctgtGGAAGACGGCACCACCGACATCACGTTACCTGCCCTCGCGCTGACGGACGC
901  -----+-----+-----+-----+-----+-----+ 960
      S S V E D G T T D I T F T C P R A D G R
      CGTGCGATGGAGATCTTGAAGAAGCTTCAGGTTCAAGGGCAACTGGACCAATGTGCTTTAC
961  -----+-----+-----+-----+-----+-----+ 1020
      R A M E I L K K L Q V Q G N W T N V L Y
      GACGACCAGGTCGGCAAAGTCTCCCTCGTGGGTGCTGGCATGAAGTCTACCCAGGTGTT
1021 -----+-----+-----+-----+-----+-----+ 1080
      D D Q V G K V S L V G A G M K S H P G V
      ACCGCAGAGTTCATGGAAGCTCTGCGCGATGTCAACGTGAACATCGAATTGATTTCCATC
1081 -----+-----+-----+-----+-----+-----+ 1140
      T A E F M E A L R D V N V N I E L I S I
      TCTGAGATCCGCATTTCCGTGCTGATCCGTGAAGATGATCTGGATGCTGCTGCACGTGCA
1141 -----+-----+-----+-----+-----+-----+ 1200
      S E I R I S V L I R E D D L D A A A R A
      TTGCATGAGCAGTTCCAGCTGGGCGGCGAAGACGAAGCCGTCGTTTATGCAGGCACCGGA
1201 -----+-----+-----+-----+-----+-----+ 1260
      L H E Q F Q L G G E D E A V V Y A G T G
      CGCTAA
1261 ----- 1266
      R *

```

FIG.3B

Nucleotide sequence of ATCC21529 asd (SEQ ID NO:3)

```
1  ATGACCACCA TCGCAGTTGT TGGTGCAACC GGCCAGGTCG GCCAGGTTAT
51  GCGCACCTTT TTGGAAGAGC GCAATTTCCC AGCTGACACT GTTCGTTTCT
101 TTGCTTCCCC GCGTTCCGCA GGCCGTAAGA TTGAATTCCG TGGCACGGAA
151 ATCGAGGTAG AAGACATTAC TCAGGCAACC GAGGAGTCCC TCAAGGGCAT
201 CGACGTTGCG TTGTTCTCTG CTGGAGGCAC CGCTTCCAAG CAGTACGCTC
251 CACTGTTTGC TGCTGCAGGC GCGACTGTTG TGGATAACTC TTCTGCTTGG
301 CGCAAGGACG ACGAGGTTCC ACTAATCGTC TCTGAGGTGA ACCCTTCCGA
351 CAAGGATTCC CTGGTCAAGG GCATTATTGC GAATCCTAAC TGCACCACCA
401 TGGCTGCAAT GCCAGTGCTG AAGCCACTGC ACGATGCCGC TGGTCTTGTA
451 AAGCTTCACG TTTCCTCTTA CCAGGCTGTT TCCGGTTCTG GTCTTGCAAG
501 TGTGGAAACC TTGGCAAAGC AGGTTGCTGC AGTTGGCGAC CACAACGTTG
551 AGTTCGTCCA TGATGGACAG GCTGCTGACG CAGGCGATGT CGGACCTTAC
601 GTTTCCCCAA TCGCTTACAA CGTGCTGCCA TTCGCCGGAA ACCTCGTCGA
651 TGACGGCACC TTCGAAACCG ACGAAGAGCA GAAGCTGCGC AACGAATCCC
701 GCAAGATTCT CGGCCTCCCA GACCTCAAGG TCTCAGGCAC CTGCGTCCGC
751 GTGCCGGTTT TCACCGGCCA CACGCTGACC ATTCACGCCG AATTCGACAA
801 GGCAATCACC GTCGAGCAGG CGCAGGAGAT CTTGGGTGCC GCTTCAGGCG
851 TCGAGCTTGT CGACGTCCCA ACCCCACTTG CAGCTGCCGG CATTGACGAA
901 TCCCTCGTTG GACGCATCCG TCAGGACTCC ACTGTCGACG ACAACCGCGG
951 TCTGGTTCTC GTCGTATCTG GCGATAACCT TCGCAAGGGC GCAGCACTGA
1001 ACACCATTCA GATTGCTGAG CTGCTGGTTA AGTAA
```

FIG. 4

Amino acid sequence of ATCC21529 asd (SEQ ID NO:4)

```

1  ATGACCACCATCGCAGTTGTTGGTGCAACCGGCCAGGTCGGCCAGGTTATGCGCACCTTT
   -----+-----+-----+-----+-----+-----+ 60
   M T T I A V V G A T G Q V G Q V M R T F
61  TTGGAAGAGCGCAATTTCCCAGCTGACACTGTTTCGTTTCTTTGCTTCCCCGCGTTCCGCA
   -----+-----+-----+-----+-----+-----+ 120
   L E E R N F P A D T V R F F A S P R S A
121 GGCCGTAAGATTGAATTCCGTGGCACGGAAATCGAGGTAGAAGACATTACTCAGGCAACC
   -----+-----+-----+-----+-----+-----+ 180
   G R K I E F R G T E I E V E D I T Q A T
181 GAGGAGTCCCTCAAGGGCATCGACGTTGCGTTGTTCTCTGCTGGAGGCACCGCTTCCAAG
   -----+-----+-----+-----+-----+-----+ 240
   E E S L K G I D V A L F S A G G T A S K
241 CAGTACGCTCCACTGTTTGCTGCTGCAGGCGCGACTGTTGTGGATAACTCTTCTGCTTGG
   -----+-----+-----+-----+-----+-----+ 300
   Q Y A P L F A A A G A T V V D N S S A W
301 CGCAAGGACGACGAGGTTCCACTAATCGTCTCTGAGGTGAACCCTTCCGACAAGGATTCC
   -----+-----+-----+-----+-----+-----+ 360
   R K D D E V P L I V S E V N P S D K D S
361 CTGGTCAAGGGCATTATTGCGAATCCTAACTGCACCACCATGGCTGCAATGCCAGTGCTG
   -----+-----+-----+-----+-----+-----+ 420
   L V K G I I A N P N C T T M A A M P V L
421 AAGCCACTGCACGATGCCGCTGGTCTTGTAAGCTTCACGTTTCCTCTTACCAGGCTGTT
   -----+-----+-----+-----+-----+-----+ 480
   K P L H D A A G L V K L H V S S Y Q A V
481 TCCGGTTCTGGTCTTGCAGGTGTGGAAACCTTGGCAAAGCAGGTTGCTGCAGTTGGCGAC
   -----+-----+-----+-----+-----+-----+ 540
   S G S G L A G V E T L A K Q V A A V G D

```

FIG.5A

CACAACGTTGAGTTCGTCCATGATGGACAGGCTGCTGACGCAGGCGATGTCGGACCTTAC
 541 -----+-----+-----+-----+-----+-----+ 600
 H N V E F V H D G Q A A D A G D V G P Y
 GTTTCCTCAATCGCTTACAACGTGCTGCCATTGCGCGGAAACCTCGTCGATGACGGCACC
 601 -----+-----+-----+-----+-----+-----+ 660
 V S P I A Y N V L P F A G N L V D D G T
 TTCGAAACCGACGAAGAGCAGAAGCTGCGCAACGAATCCCGCAAGATTCTCGGCCTCCCA
 661 -----+-----+-----+-----+-----+-----+ 720
 F E T D E E Q K L R N E S R K I L G L P
 GACCTCAAGGTCTCAGGCACCTGCGTCCGCGTGCCGGTTTTACCGGCCACACGCTGACC
 721 -----+-----+-----+-----+-----+-----+ 780
 D L K V S G T C V R V P V F T G H T L T
 ATTCACGCCGAATTCGACAAGGCAATCACCGTCGAGCAGGCGCAGGAGATCTTGGGTGCC
 781 -----+-----+-----+-----+-----+-----+ 840
 I H A E F D K A I T V E Q A Q E I L G A
 GCTTCAGGCGTCGAGCTTGTCGACGTCCCAACCCCACTTGCGAGCTGCCGGCATTGACGAA
 841 -----+-----+-----+-----+-----+-----+ 900
 A S G V E L V D V P T P L A A A G I D E
 TCCCTCGTTGGACGCATCCGTCAGGACTCCACTGTCGACGACAACCGCGGTCTGGTTCTC
 901 -----+-----+-----+-----+-----+-----+ 960
 S L V G R I R Q D S T V D D N R G L V L
 GTCGTATCTGGCGATAACCTTCGCAAGGGCGCAGCACTGAACACCATTGAGATTGCTGAG
 961 -----+-----+-----+-----+-----+-----+ 1020
 V V S G D N L R K G A A L N T I Q I A E
 CTGCTGGTTAAGTAA
 1021 -----+----- 1035
 L L V K *

FIG.5B

Nucleotide sequence of dapA (SEQ ID NO:5)

```
1  ATGAGCACAG GTTTAACAGC TAAGACCGGA GTAGAGCACT TCGGCACCGT
51  TGGAGTAGCA ATGGTTACTC CATTACGGA ATCCGGAGAC ATCGATATCG
101 CTGCTGGCCG CGAAGTCGCG GCTTATTTGG TTGATAAGGG CTTGGATTCT
151 TTGGTTCTCG CGGGCACCAC TGGTGAATCC CCAACGACAA CCGCCGCTGA
201 AAAACTAGAA CTGCTCAAGG CCGTTCGTGA GGAAGTTGGG GATCGGGCGA
251 AGCTCATCGC CGGTGTCGGA ACCAACAACA CGCGGACATC TGTGGAACCT
301 GCGGAAGCTG CTGCTTCTGC TGGCGCAGAC GGCCTTTTAG TTGTAACCTC
351 TTATTACTCC AAGCCGAGCC AAGAGGGATT GCTGGCGCAC TTCGGTGCAA
401 TTGCTGCAGC AACAGAGGTT CCAATTTGTC TCTATGACAT TCCTGGTCGG
451 TCAGGTATTC CAATTGAATC TGATACCATG AGACGCCTGA GTGAATTACC
501 TACGATTTTG GCGGTCAAGG ACGCCAAGGG TGACCTCGTT GCAGCCACGT
551 CATTGATCAA AGAAACGGGA CTTGCCTGGT ATTCAGGCGA TGACCCACTA
601 AACCTTGTTT GGCTTGCTTT GGGCGGATCA GGTTTCATTT CCGTAATTGG
651 ACATGCAGCC CCCACAGCAT TACGTGAGTT GTACACAAGC TTCGAGGAAG
701 GCGACCTCGT CCGTGCGCGG GAAATCAACG CCAAACATC ACCGCTGGTA
751 GCTGCCCAAG GTCGCTTGGG TGGAGTCAGC TTGGCAAAAG CTGCTcTGCG
801 TCTGCAGGGC ATCAACGTAG GAGATCCTCG ACTTCCAATT ATGGCTCCAA
851 ATGAGCAGGA ACTTGAGGCT CTCCGAGAAG ACATGAAAAA AGCTGGAGTT
901 CTATAA
```

FIG. 6

Amino acid sequence of dapA (SEQ ID NO:6)

```
ATGAGCACAGGTTTAACAGCTAAGACCGGAGTAGAGCACTTCGGCACCGTTGGAGTAGCA
1  -----+-----+-----+-----+-----+-----+ 60
  M S T G L T A K T G V E H F G T V G V A

ATGGTTACTCCATTCACGGAATCCGGAGACATCGATATCGCTGCTGGCCGCGAAGTCGCG
61  -----+-----+-----+-----+-----+-----+ 120
  M V T P F T E S G D I D I A A G R E V A

GCTTATTTGGTTGATAAGGGCTTGGATTCTTTGGTTCTCGCGGGCACCCTGGTGAATCC
121 -----+-----+-----+-----+-----+-----+ 180
  A Y L V D K G L D S L V L A G T T G E S

CCAACGACAACCGCCGCTGAAAACTAGAACTGCTCAAGGCCGTTCTGTGAGGAAGTTGGG
181 -----+-----+-----+-----+-----+-----+ 240
  P T T T A A E K L E L L K A V R E E V G

GATCGGGCGAAGCTCATCGCCGGTGTGGAACCAACAACACGCGGACATCTGTGGAACCT
241 -----+-----+-----+-----+-----+-----+ 300
  D R A K L I A G V G T N N T R T S V E L

GCGGAAGCTGCTGCTTCTGCTGGCGCAGACGGCCTTTTAGTTGTAACCTTATTACTCC
301 -----+-----+-----+-----+-----+-----+ 360
  A E A A A S A G A D G L L V V T P Y Y S

AAGCCGAGCCAAGAGGGATTGCTGGCGCACTTCGGTGCAATTGCTGCAGCAACAGAGGTT
361 -----+-----+-----+-----+-----+-----+ 420
  K P S Q E G L L A H F G A I A A A T E V

CCAATTTGTCTCTATGACATTCCTGGTCGGTCAGGTATTCCAATTGAATCTGATACCATG
421 -----+-----+-----+-----+-----+-----+ 480
  P I C L Y D I P G R S G I P I E S D T M
```

FIG.7A

AGACGCCTGAGTGAATTACCTACGATTTTGGCGGTCAAGGACGCCAAGGGTGACCTCGTT
 481 -----+-----+-----+-----+-----+-----+ 540
 R R L S E L P T I L A V K D A K G D L V
 GCAGCCACGTCATTGATCAAAGAAACGGGACTTGCCTGGTATTCAGGCGATGACCCACTA
 541 -----+-----+-----+-----+-----+-----+ 600
 A A T S L I K E T G L A W Y S G D D P L
 AACCTTGTTTGGCTTGCTTTGGGCGGATCAGGTTTCATTTCCGTAATTGGACATGCAGCC
 601 -----+-----+-----+-----+-----+-----+ 660
 N L V W L A L G G S G F I S V I G H A A
 CCCACAGCATTACGTGAGTTGTACACAAGCTTCGAGGAAGGCGACCTCGTCCGTGCGCGG
 661 -----+-----+-----+-----+-----+-----+ 720
 P T A L R E L Y T S F E E G D L V R A R
 GAAATCAACGCCAAACTATCACCGCTGGTAGCTGCCCAAGGTCGCTTGGGTGGAGTCAGC
 721 -----+-----+-----+-----+-----+-----+ 780
 E I N A K L S P L V A A Q G R L G G V S
 TTGGCAAAAGCTGCTcTGCCTCTGCAGGGCATCAACGTAGGAGATCCTCGACTTCCAATT
 781 -----+-----+-----+-----+-----+-----+ 840
 L A K A A L R L Q G I N V G D P R L P I
 ATGGCTCCAAATGAGCAGGAACTTGAGGCTCTCCGAGAAGACATGAAAAAAGCTGGAGTT
 841 -----+-----+-----+-----+-----+-----+ 900
 M A P N E Q E L E A L R E D M K K A G V
 CTATAA
 901 ----- 906
 L * -

FIG.7B

Nucleotide sequence of dapB (SEQ ID NO:7)

```
1  ATGGGAATCA AGGTTGGCGT TCTCGGAGCC AAAGGCCGTG TTGGTCAAAC
51  TATTGTGGCA GCAGTCAATG AGTCCGACGA TCTGGAGCTT GTTGCAGAGA
101 TCGGCGTCGA CGATGATTTG AGCCTTCTGG TAGACAACGG CGCTGAAGTT
151 GTCGTTGACT TCACCACTCC TAACGCTGTG ATGGGCAACC TGGAGTTCTG
201 CATCAACAAC GGCATTTCTG CGGTTGTTGG AACCACGGGC TTCGATaATG
251 CTCGTTTGGG GCAGGTTTCGC GcCTGGCTTG AAGGAAAAGA CAATGTCGGT
301 GTTCTGATCG CACCTAACTT TGCTATCTCT GCGGTGTTGA CCATGGTCTT
351 TTCCAAGCAG GCTGCCCCGT TCTTCGAATC AGCTGAAGTT ATTGAGCTGC
401 ACCACCCCAA CAAGCTGGAT GCACCTTCAG GCACCGCGAT CCACACTGCT
451 CAGGGCATTG CTGCGGCACG CAAAGAAGCA GGCATGGACG CACAGCCAGA
501 TGCACCGAG CAGGCACTTG AGGGTTCCCG TGGCGCAAGC GTAGATGGAA
551 TCCCaGTTCA cGCAGTCCGC ATGTCCGGCA TGGTTGCTCA CGAGCAAGTT
601 ATCTTTGGCA CCCAGGGTCA GACCTTGACC ATCAAGCAGG ACTCCTATGA
651 TCGCAACTCA TTTGCACCAG GTGTCTTGGT GGGTGTGCGC AACATTGCAC
701 AGCACCCAGG CCTAGTCGTA GGACTTGAGC ATTACCTAGG CCTGTAA
```

FIG. 8

Amino acid sequence of dapB (SEQ ID NO:8)

ATGGGAATCAAGGTTGGCGTTCTCGGAGCCAAAGGCCGTGTTGGTCAAACCTATTGTGGCA
1 -----+-----+-----+-----+-----+-----+ 60
M G I K V G V L G A K G R V G Q T I V A
GCAGTCAATGAGTCCGACGATCTGGAGCTTGTTGCAGAGATCGGCGTCGACGATGATTTG
61 -----+-----+-----+-----+-----+-----+ 120
A V N E S D D L E L V A E I G V D D D L
AGCCTTCTGGTAGACAACGGCGCTGAAGTTGTCGTTGACTTCACCACTCCTAACGCTGTG
121 -----+-----+-----+-----+-----+-----+ 180
S L L V D N G A E V V V D F T T P N A V
ATGGGCAACCTGGAGTTCTGCATCAACAACGGCATTCTGCGGTTGTTGGAACCACGGGC
181 -----+-----+-----+-----+-----+-----+ 240
M G N L E F C I N N G I S A V V G T T G
TTCGATaATGCTCGTTTGGAGCAGGTTGCGGcCTGGCTTGAAGGAAAAGACAATGTCGGT
241 -----+-----+-----+-----+-----+-----+ 300
F D N A R L E Q V R A W L E G K D N V G
GTTCTGATCGCACCTAACTTTGCTATCTCTGCGGTGTTGACCATGGTCTTTTCCAAGCAG
301 -----+-----+-----+-----+-----+-----+ 360
V L I A P N F A I S A V L T M V F S K Q
GCTGCCCGCTTCTTCGAATCAGCTGAAGTTATTGAGCTGCACCACCCCAACAAGCTGGAT
361 -----+-----+-----+-----+-----+-----+ 420
A A R F F E S A E V I E L H H P N K L D

FIG.9A

GCACCTTCAGGCACCGCGATCCACACTGCTCAGGGCATTGCTGCGGCACGCAAAGAAGCA
 421+.....+.....+.....+.....+.....+ 480
 A P S G T A I H T A Q G I A A A R K E A
 GGCATGGACGCACAGCCAGATGCGACCGAGCAGGCACTTGAGGGTTCCTGGCGCAAGC
 481+.....+.....+.....+.....+.....+ 540
 G M D A Q P D A T E Q A L E G S R G A S
 GTAGATGGAATCCCaGTTCAcGCAGTCCGCATGTCCGGCATGGTTGCTCACGAGCAAGTT
 541+.....+.....+.....+.....+.....+ 600
 V D G I P V H A V R M S G M V A H E Q V
 ATCTTTGGCACCAGGGTCAGACCTTGACCATCAAGCAGGACTCCTATGATCGCAACTCA
 601+.....+.....+.....+.....+.....+ 660
 I F G T Q G Q T L T I K Q D S Y D R N S
 TTTGCACCAGGTGTCTTGGTGGGTGTGCGCAACATTGCACAGCACCCAGGCCTAGTCGTA
 661+.....+.....+.....+.....+.....+ 720
 F A P G V L V G V R N I A Q H P G L V V
 GGACTTGAGCATTACCTAGGCCTGTAA
 721+.....+..... 747
 G L E H Y L G L *

FIG.9B

Nucleotide sequence of ddh (SEQ ID NO:9)

```

1  ATGCATTTTCG GTAAGCTCGA CCAGGACAGT GCCACCACAA TTTTGGAGGA
51  TTACAAGAAC  ATGACCAACA TCCGCGTAGC TATCGTaGGC TACGGAAACC
101 TGGGACGCAG  CGTCGAAAAG CTTATTGCCA AGCAGCCCGA CATGGACCTT
151 GTAGGAATCT  TCTCGCGCCG GGCCACCCTC GACACAAAGA CGCCAGTCTT
201 TGATGTCGCC  GACGTGGACA AGCACGCCGA CGACGTGGAC GTGCTGTTCC
251 TGTGCATGGG  CTCCGCCACC GACATCCCTG AGCAGGCACC AAAGTTCGCG
301 CAGTTCGCCT  GCACCGTAGA CACCTACGAC AACCACCGCG ACATCCCACG
351 CCACCGCCAG  GTCATGAACG AAGCCGCCAC CGCAGCCGGC AACGTTGCAC
401 TGGTCTCTAC  CGGCTGGGAT CCAGGAATGT TCTCCATCAA CCGCGTCTAC
451 GCAGCGGCAG  TCTTAGCCGA GCACCAGCAG CACACCTTCT GGGGCCCAGG
501 TTTGTCACAG  GGCCACTCCG ATGCTTTGCG ACGCATCCCT GGC GTTCAAA
551 AGGCcGTCCA GTACACCCTC CCATCCGAAG AaGCCCTGGA AAAGGCCCGC
601 CGTGGCGAAG  CCGGCGACCT cACCGGAAAG CAAACCCACA AGCGCCAATG
651 CTTCGTGGTT  GCCGACGCGG CCGAcCACGA GCGCATCGAA AACGACATCC
701 GCACCATGCC  TGATTACTTC GTTGGCTACG AAGTCGAAGT CAACTTCATC
751 GACGAAGCAA  CCTTgGACgC CGAGCACACC GGCATGCCAC ACGGcGGaCA
801 CGTGATcACC  ACCGGCGACA CCGGTGGCTT CAACCACACC GTGGAATACA
851 TCCTgAAGCT  GGACCGAAAC CCAGATTTCa CCGCTTctTC ACAGATCGCT
901 TTCGGcCGCG  CAGCTCACCG CATGAAGCAG CAGGGCCAAA GCGGtGCTTT
951 CACCGTCCTC  GAAGTTGCTC CATActTGCT CTCCCCgGAG AACTTGGAtG
1001 ATCTGATCGC  ACGCGACGTC TAA

```

FIG. 10

Amino acid sequence of ddh (SEQ ID NO:10)

```
ATGCATTTTCGGTAAGCTCGACCAGGACAGTGCCACCACAATTTTGGAGGATTACAAGAAC
1  .....+.....+.....+.....+.....+.....+.....+ 60
  M H F G K L D Q D S A T T I L E D Y K N
ATGACCAACATCCGCGTAGCTATCGTaGGCTACGGAAACCTGGGACGCAGCGTCGAAAAG
61  .....+.....+.....+.....+.....+.....+.....+ 120
  M T N I R V A I V G Y G N L G R S V E K
CTTATTGCCAAGCAGCCCGACATGGACCTTGTAGGAATCTTCTCGCGCCGGGCCACCCTC
121 .....+.....+.....+.....+.....+.....+.....+ 180
  L I A K Q P D M D L V G I F S R R A T L
GACACAAAGACGCCAGTCTTTGATGTCGCCGACGTGGACAAGCACGCCGACGACGTGGAC
181 .....+.....+.....+.....+.....+.....+.....+ 240
  D T K T P V F D V A D V D K H A D D V D
GTGCTGTTTCCTGTGCATGGGCTCCGCCACCGACATCCCTGAGCAGGCACCAAAGTTCGCG
241 .....+.....+.....+.....+.....+.....+.....+ 300
  V L F L C M G S A T D I P E Q A P K F A
CAGTTCGCCTGCACCGTAGACACCTACGACAACCACCGCGACATCCCACGCCACCGCCAG
301 .....+.....+.....+.....+.....+.....+.....+ 360
  Q F A C T V D T Y D N H R D I P R H R Q
GTCATGAACGAAGCCGCCACCGCAGCCGGCAACGTTGCACTGGTCTCTACCGGCTGGGAT
361 .....+.....+.....+.....+.....+.....+.....+ 420
  V M N E A A T A A G N V A L V S T G W D
CCAGGAATGTTCTCCATCAACCGCGTCTACGCAGCGGCAGTCTTAGCCGAGCACCAGCAG
421 .....+.....+.....+.....+.....+.....+.....+ 480
  P G M F S I N R V Y A A A V L A E H Q Q
CACACCTTCTGGGGCCAGGTTTGTACAGGGCCACTCCGATGCTTTGCGACGCATCCCT
481 .....+.....+.....+.....+.....+.....+.....+ 540
  H T F W G P G L S Q G H S D A L R R I P
```

FIG.11A

GGCGTTCAAAAGGCcGTCCAGTACACCCTCCCATCCGAAGaAGCCCTGGAAAAGGCCCGC
541 -----+-----+-----+-----+-----+-----+ 600
G V Q K A V Q Y T L P S E E A L E K A R
CGTGGCGAAGCCGGCGACCTcACCGGAAAGCAAACCCACAAGCGCCAATGCTTCGTGGTT
601 -----+-----+-----+-----+-----+-----+ 660
R G E A G D L T G K Q T H K R Q C F V V
GCCGACGCGGCCGAcCACGAGCGCATCGAAAACGACATCCGCACCATGCCTGATTACTTC
661 -----+-----+-----+-----+-----+-----+ 720
A D A A D H E R I E N D I R T M P D Y F
GTTGGCTACGAAGTCGAAGTCAACTTCATCGACGAAGCAACCTTgGACgCCGAGCACACC
721 -----+-----+-----+-----+-----+-----+ 780
V G Y E V E V N F I D E A T L D A E H T
GGCATGCCACACGGcGGaCACGTGATcACCACCGGCGACACCGGTGGCTTCAACCACACC
781 -----+-----+-----+-----+-----+-----+ 840
G M P H G G H V I T T G D T G G F N H T
GTGGAATACATCCTgAAGCTGGACCGAAACCCAGATTTACCGCTTctTCACAGATCGCT
841 -----+-----+-----+-----+-----+-----+ 900
V E Y I L K L D R N P D F T A S S Q I A
TTCGGcCGCGCAGCTCACCGCATGAAGCAGCAGGGCCAAAGCGGtGCTTTACCGTCCTC
901 -----+-----+-----+-----+-----+-----+ 960
F G R A A H R M K Q Q G Q S G A F T V L
GAAGTTGCTCCATACTTGCTCTCCCCgGAGAACTTGGAtGATCTGATCGCACGCGACGTC
961 -----+-----+-----+-----+-----+-----+ 1020
E V A P Y L L S P E N L D D L I A R D V
TAA
1021 --- 1023

FIG.11B

Sequence of full length LysA from NRRL B-11474 (SEQ ID NO: 11);
Underlined region: the priming site for lysA primer

ATGGCTACAGTTGAAAATTTCAATGAACTTCCCGCACACGTATGGCCACGCAATGCAGTG
CGCCAAGAAGACGGCGTTGTACCGTCGCTGGTGTGCCTCTGCCTGACCTCGCTGAAGAA
TACGGAACCCCACTGTTTCGTAGTCGACGAGGACGATTTCCGTTCCCGCTGTCGCGACATG
GCTACCGCATTCCGGTGGACCAGGCAATGTGCACTACGCATCCAAAGCGTTTCCTGACCAAG
ACCATTGCACGTTGGGTTGATGAAGAGGGGCTGGCACTGGACATTGCGTCCATCAATGAA
CTGGGCATTGCCCTGGCCGCTGGTTTTCCCGGCCAGCCGTATCACCGCGCACGGCAACAAC
AAAGGCGTAGAGTTCTGCGCGCGTTGGTTCAAACGGTGTGCGGCATGTGGTGTCTGGAC
TCCGCGCAGGAATTGGAACCTGCTGGATTACGTTGCCGCTGGTGAAGGCAAGATCCAGGAC
GTGTTGATCCGCGTGAAGCCAGGTATCGAAGCCACACCCACGAGTTCATCGCCACTAGC
CACGAAGACCAGAAGTTCGGATTCTCCCTGGCATCCGGTTCGCGATTCTGAAGCAGCGAAA
GCAGCCAACAATGCAGAGAACTTGAACCTGGTTGGTCTGCACTGCCATGTTGGTTCCCAG
GTGTTTCGACGCCGAAGGCTTCAAGCTGGCAGCAGAGCGCGTGTGGGCCTGTACTCACAG
ATCCACAGCGAACTAGGTGTCGCCCTTCCTGAGCTGGACCTCGGTGGCGGATACGGCATC
GCCTACACTGCAGATGAGGAACCACTCAACGTCGCGAGAAGTCGCCTCCGACCTACTCACC
GCAGTCGGAAAAATGGCAGCGGAACTAGGCATCGACGCACCAACCGTGCTTGTTGAGCCC
GGCCGCGCTATCGCAGGCCCTCCACCGTGACCATCTACGAAGTCGGCACCACCAAAAAC
GTCCACGTAGACGACGACAAAACCCGCCGCTACGTAGCCGTCGACGGAGGCATGTCCGAC
AACATCCGCCCAGCACTCTACGGCTCCGAATACGACGCCCGCGTAGTATCCCGCTTCGCC
GAAGGAGACCCAGTAAGCACCCGCATCGTGGGCTCCCACTGCGAATCCGGCGATATCCTG
ATCAACGATGAAATCTACCCATCTGACATCACCAGCGGCGACTTCCTCGCACTCGCAGCC
ACCGGCGCATACTGCTACGCCATGAGCTCCCGCTACAACGCCTTCACACGGCCCCGCCGTC
GTGTCCGTCCGCGCTGGCAGCTCCCGCCTCATGCTGCGCCGCGAAACCCTCGACGACATC
CTCTCACTAGAGGCATAA

FIG.12

Full length sequence of LysA (NRRL-B11474)
DIAMINOPIMELATE DECARBOXYLASE (Lys A) (SEQ ID NO:12)

MATVENFNELPAHVWPRNAVRQEDGVVTVAGVPLPDLAEEYGTPLFVVDEDDFRSRCRDM
ATAFGGPGNVHYASKAFLTKTIARWVDEEGLALDIASINELGIALAAGFPASRITAHGNN
KGVEFLRALVQNGVGHVVLDQAQELLDYVAAGEGKIQDVLIRVKPGIEAHTHEFIATS
HEDQKFGFSLASGSAFEAAKAANNAENLNLVGLHCHVGSQVFDAEGFKLAAERVLGLYSQ
IHSELGVALPELDLGGGYGIAYTADEEPLNVAEVASDLLTAVGKMAAELGIDAPTVLVEP
GRAIAGPSTVTIYEVGTTKNVHVDDDKTRRYVAVDGGMSDNIRPALYGSEYDARVVSRFA
EGDPVSTRIVGSHCESGDILINDEIYPSDITSGDFLAATGAYCYAMSSRYNAFTRPAV
VSVRAGSSRLMLRRETLDLILSLEA

FIG. 13

Nucleotide sequence of AS019 *lysA* (SEQ ID NO:13) (pRS6)

```
1  ATGGCTACAG TTGAAAATTT CAATGAACTT CCCGCACACG TATGGCCACG
51  CAATGCCGTG CGCCAAGAAG ACGGCGTTGT CACCGTCGCT GGTGTGCCTC
101 TGCCTGACCT CGCTGAAGAA TACGGAACCC CACTGTTCGT AGTCGACGAG
151 GACGATTTCC GTTCCCGCTG TCGCGACATG GCTACCGCAT TCGGTGGACC
201 AGGCAATGTG CACTACGCAT CTAAAGCGTT CCTGACCAAG ACCATTGCAC
251 GTTGGGTTGA TGAAGAGGGG CTGGCACTGG ACATTGCATC CATCAACGAA
301 CTGGGCATTG CCCTGGCCGC TGGTTTCCCC GCCAGCCGTA TCACCGCGCA
351 CGGCAACAAC AAAGGCGTAG AGTTCCTGCG CGCGTTGGTT CAAAACGGTG
401 TGGGACACGT GGTGCTGGAC TCCGCACAGG AACTAGAACT GTTGGATTAC
451 GTTGCCGCTG GTGAAGGCAA GATTCAGGAC GTGTTGATCC GCGTAAAGCC
501 AGGCATCGAA GCACACACCC ACGAGTTCAT CGCCACTAGC CACGAAGACC
551 AGAAGTTCGG ATTCTCCCTG GCATCCGGTT CCGCATTCTGA AGCAGCAAAA
601 GCCGCCAACA ACGCAGAAAA CCTGAACCTG GTTGGCCTGC ACTGCCACGT
651 TGGTTCCCAG GTGTTTCGACG CCGAAGGCTT CAAGCTGGCA GCAGAACGCG
701 TGTTGGGCCT GTACTCACAG ATCCACAGCG AACTGGGCGT TGCCCTTCCT
751 GAACTGGATC TCGGTGGCGG ATACGGCATT GCCTATACCG CAGCTGAAGA
801 ACCACTCAAC GTCGCAGAAG TTGCCTCCGA CCTGCTCACC GCAGTCGGAA
851 AAATGGCAGC GGAAGTAGGC ATCGACGCAC CAACCGTGCT TGTTGAGCCC
901 GGCCGCGCTA TCGCAGGCCC CTCCACCGTG ACCATCTACG AAGTCGGCAC
951 CACCAAAGAC GTCCACGTAG ACGACGACAA AACCCGCCGT TACATCGCCG
1001 TGGACGGAGG CATGTCCGAC AACATCCGCC CAGCACTCTA CGGCTCCGAA
1051 TACGACGCCC GCGTAGTATC CCGCTTCGCC GAAGGAGACC CAGTAAGCAC
1101 CCGCATCGTG GGCTCCCACT GCGAATCCGG CGATATCCTG ATCAACGATG
1151 AAATCTACCC ATCTGACATC ACCAGCGGCG ACTTCCTTGC ACTCGCAGCC
1201 ACCGGCGCAT ACTGCTACGC CATGAGCTCC CGCTACAACG CCTTCACACG
1251 GCCCGCCGTC GTGTCCGTCC GCGCTGGCAG CTCCCGCCTC ATGCTGCGCC
1301 GCGAAACGCT CGACGACATC CTCTCACTAG AGGCATAA
```

FIG.14

Full length amino acid sequence of lysA (pRS6)(SEQ ID NO:14)

```
ATGGCTACAGTTGAAAATTTCAATGAACTTCCCGCACACGTATGGCCACGCAATGCCGTG
1  -----+-----+-----+-----+-----+-----+ 60
  M A T V E N F N E L P A H V W P R N A V

CGCCAAGAAGACGGCGTTGTCACCGTCGCTGGTGTGCCTCTGCCTGACCTCGCTGAAGAA
61  -----+-----+-----+-----+-----+-----+ 120
  R Q E D G V V T V A G V P L P D L A E E

TACGGAACCCCACTGTTTCGTAGTCGACGAGGACGATTTCCGTTCCCGCTGTCGCGACATG
121 -----+-----+-----+-----+-----+-----+ 180
  Y G T P L F V V D E D D F R S R C R D M

GCTACCGCATTTCGGTGGACCAGGCAATGTGCACTACGCATCTAAAGCGTTCCTGACCAAG
181 -----+-----+-----+-----+-----+-----+ 240
  A T A F G G P G N V H Y A S K A F L T K

ACCATTCACGTTGGGTTGATGAAGAGGGGCTGGCACTGGACATTGCATCCATCAACGAA
241 -----+-----+-----+-----+-----+-----+ 300
  T I A R W V D E E G L A L D I A S I N E

CTGGGCATTGCCCTGGCCGCTGGTTTCCCCGCCAGCCGTATCACCGCGCACGGCAACAAC
301 -----+-----+-----+-----+-----+-----+ 360
  L G I A L A A G F P A S R I T A H G N N

AAAGGCGTAGAGTTCCTGCGCGCGTTGGTTCAAAACGGTGTGGGACACGTGGTGCTGGAC
361 -----+-----+-----+-----+-----+-----+ 420
  K G V E F L R A L V Q N G V G H V V L D

TCCGCACAGGAACTAGAACTGTTGGATTACGTTGCCGCTGGTGAAGGCAAGATTCAGGAC
421 -----+-----+-----+-----+-----+-----+ 480
  S A Q E L E L L D Y V A A G E G K I Q D
```

FIG.15A

GTGTTGATCCGCGTAAAGCCAGGCATCGAAGCACACACCCACGAGTTCATCGCCACTAGC
 481 -----+-----+-----+-----+-----+-----+ 540
 V L I R V K P G I E A H T H E F I A T S
 CACGAAGACCAGAAGTTCGGATTCTCCCTGGCATCCGGTTCGCGATTCTGAAGCAGCAAAA
 541 -----+-----+-----+-----+-----+-----+ 600
 H E D Q K F G F S L A S G S A F E A A K
 GCCGCCAACAACGCAGAAAACCTGAACCTGGTTGGCCTGCACTGCCACGTTGGTTCCCAG
 601 -----+-----+-----+-----+-----+-----+ 660
 A A N N A E N L N L V G L H C H V G S Q
 GTGTTGACGCCGAAGGCTTCAAGCTGGCAGCAGAACGCGTGTGGGCCTGTACTCACAG
 661 -----+-----+-----+-----+-----+-----+ 720
 V F D A E G F K L A A E R V L G L Y S Q
 ATCCACAGCGAACTGGGCGTTGCCCTTCCTGAACTGGATCTCGGTGGCGGATACGGCATT
 721 -----+-----+-----+-----+-----+-----+ 780
 I H S E L G V A L P E L D L G G G Y G I
 GCCTATACCGCAGCTGAAGAACCACTCAACGTGCGAGAAGTTGCCTCCGACCTGCTCACC
 781 -----+-----+-----+-----+-----+-----+ 840
 A Y T A A E E P L N V A E V A S D L L T
 GCAGTCGGAAAAATGGCAGCGGAACTAGGCATCGACGCACCAACCGTGCTTGTTGAGCCC
 841 -----+-----+-----+-----+-----+-----+ 900
 A V G K M A A E L G I D A P T V L V E P
 GGCCGCGCTATCGCAGGCCCTCCACCGTGACCATCTACGAAGTCGGCACCACCAAAGAC
 901 -----+-----+-----+-----+-----+-----+ 960
 G R A I A G P S T V T I Y E V G T T K D

FIG.15B

GTCCACGTAGACGACGACAAAACCCGCCGTTACATCGCCGTGGACGGAGGCATGTCCGAC
 961 -----+-----+-----+-----+-----+-----+ 1020
 V H V D D D K T R R Y I A V D G G M S D
 AACATCCGCCCAGCACTCTACGGCTCCGAATACGACGCCCGCGTAGTATCCCGCTTCGCC
 1021 -----+-----+-----+-----+-----+-----+ 1080
 N I R P A L Y G S E Y D A R V V S R F A
 GAAGGAGACCCAGTAAGCACCCGCATCGTGGGCTCCCACTGCGAATCCGGCGATATCCTG
 1081 -----+-----+-----+-----+-----+-----+ 1140
 E G D P V S T R I V G S H C E S G D I L
 ATCAACGATGAAATCTACCCATCTGACATCACCAGCGGCGACTTCCTTGCACTCGCAGCC
 1141 -----+-----+-----+-----+-----+-----+ 1200
 I N D E I Y P S D I T S G D F L A L A A
 ACCGGCGCATACTGCTACGCCATGAGCTCCCGCTACAACGCCTTCACACGGCCCGCCGTC
 1201 -----+-----+-----+-----+-----+-----+ 1260
 T G A Y C Y A M S S R Y N A F T R P A V
 GTGTCCGTCCGCGCTGGCAGCTCCCGCCTCATGCTGCGCCGCGAAACGCTCGACGACATC
 1261 -----+-----+-----+-----+-----+-----+ 1320
 V S V R A G S S R L M L R R E T L D D I
 CTCTCACTAGAGGCATAA
 1321 -----+----- 1338
 L S L E A *

FIG.15C

Nucleotide sequence of orf2 in dapBA operon (SEQ ID NO:15)

```
1  GTGGCCGAAC AAGTTAAATT GAGCGTGGAG TTGATAGCGT GCAGTTCTTT
51  TACTCCACCC GCTGATGTTG AGTGGTCAAC TGATGTTGAG GGC GCGGAAG
101 CACTCGTCGA GTTTGCGGGT CGTGCCTGCT ACGAAACTTT TGATAAGCCG
151 AACCTCGAA CTGCTTCCAA TGCTGCGTAT CTGCGCCACA TCATGGAAGT
201 GGGGCACACT GCTTTGCTTG AGCATGCCAA TGCCACGATG TATATCCGAG
251 GCATTTCTCG GTCCGCGACC CATGAATTGG TCCGACACCG CCATTTTTC
301 TTCTCTCAAC TGTCTCAGCG TTTCGTGCAC AGCGGAGAAT CGGAAGTAGT
351 GGTGCCCCACT CTCATCGATG AAGATCCGCA GTTGCGTGAA CTTTTCATGC
401 ACGCCATGGA TGAGTCTCGG TTCGCTTTCA ATGAGCTGCT TAATGCGCTG
451 GAAGAAAAAC TTGGCGATGA ACCGAATGCA CTTTAAAGGA AAAAGCAGGC
501 TCGTCAAGCA GCTCGCGCTG TGCTGCCCAA CGCTACAGAG TCCAGAATCG
551 TGGTGTCTGG AAATTCCGC ACCTGGAGGC ATTTATTGG CATGCGAGCC
601 AGTGAACATG CAGACGTCGA AATCCGCGAA GTAGCGGTAG GATGTTTAAG
651 AAAGCTGCAG GTAGCAGCGC CAACTGTTTT CGGTGATTTT GAGATTGAAA
701 CTTTGGCAGA CGGATCGCAA ATGGCAACAA GCCCGTATGT CATGGACTTT
751 TAA
```

FIG.16

ORF2 amino acid sequence (SEQ ID NO:16)

```
GTGGCCGAACAAGTTAAATTGAGCGTGGAGTTGATAGCGTGCAGTTCTTTTACTCCACCC
1  -----+-----+-----+-----+-----+-----+ 60
  M A E Q V K L S V E L I A C S S F T P P

GCTGATGTTGAGTGGTCAACTGATGTTGAGGGCGCGGAAGCACTCGTCGAGTTTGCGGGT
61  -----+-----+-----+-----+-----+-----+ 120
  A D V E W S T D V E G A E A L V E F A G

CGTGCCTGCTACGAACTTTTGATAAGCCGAACCCTCGAACTGCTTCCAATGCTGCGTAT
121 -----+-----+-----+-----+-----+-----+ 180
  R A C Y E T F D K P N P R T A S N A A Y

CTGCGCCACATCATGGAAGTGGGGCACACTGCTTTGCTTGAGCATGCCAATGCCACGATG
181 -----+-----+-----+-----+-----+-----+ 240
  L R H I M E V G H T A L L E H A N A T M

TATATCCGAGGCATTTCTCGGTCCGCGACCCATGAATTGGTCCGACACCGCCATTTTTCC
241 -----+-----+-----+-----+-----+-----+ 300
  Y I R G I S R S A T H E L V R H R H F S

TTCTCTCAACTGTCTCAGCGTTTCGTGCACAGCGGAGAATCGGAAGTAGTGGTGCCCACT
301 -----+-----+-----+-----+-----+-----+ 360
  F S Q L S Q R F V H S G E S E V V V P T

CTCATCGATGAAGATCCGCAGTTGCGTGAACTTTTTCATGCACGCCATGGATGAGTCTCGG
361 -----+-----+-----+-----+-----+-----+ 420
  L I D E D P Q L R E L F M H A M D E S R
```

FIG.17A

TTCGCTTTCAATGAGCTGCTTAATGCGCTGGAAGAAAACTTGGCGATGAACCGAATGCA
 421 -----+-----+-----+-----+-----+-----+ 480
 F A F N E L L N A L E E K L G D E P N A
 CTTTAAAGGAAAAAGCAGGCTCGTCAAGCAGCTCGCGCTGTGCTGCCCAACGCTACAGAG
 481 -----+-----+-----+-----+-----+-----+ 540
 L L R K K Q A R Q A A R A V L P N A T E
 TCCAGAATCGTGGTGTCTGGAACTTCCGCACCTGGAGGCATTTTCATTGGCATGCGAGCC
 541 -----+-----+-----+-----+-----+-----+ 600
 S R I V V S G N F R T W R H F I G M R A
 AGTGAACATGCAGACGTGCAAATCCGCGAAGTAGCGGTAGGATGTTTAAGAAAGCTGCAG
 601 -----+-----+-----+-----+-----+-----+ 660
 S E H A D V E I R E V A V G C L R K L Q
 GTAGCAGCGCCAACTGTTTTCGGTGATTTTGAGATTGAACTTTGGCAGACGGATCGCAA
 661 -----+-----+-----+-----+-----+-----+ 720
 V A A P T V F G D F E I E T L A D G S Q
 ATGGCAACAAGCCCGTATGTCATGGACTTTTAA
 721 -----+-----+-----+-----+ 753
 M A T S P Y V M D F *

FIG. 17B

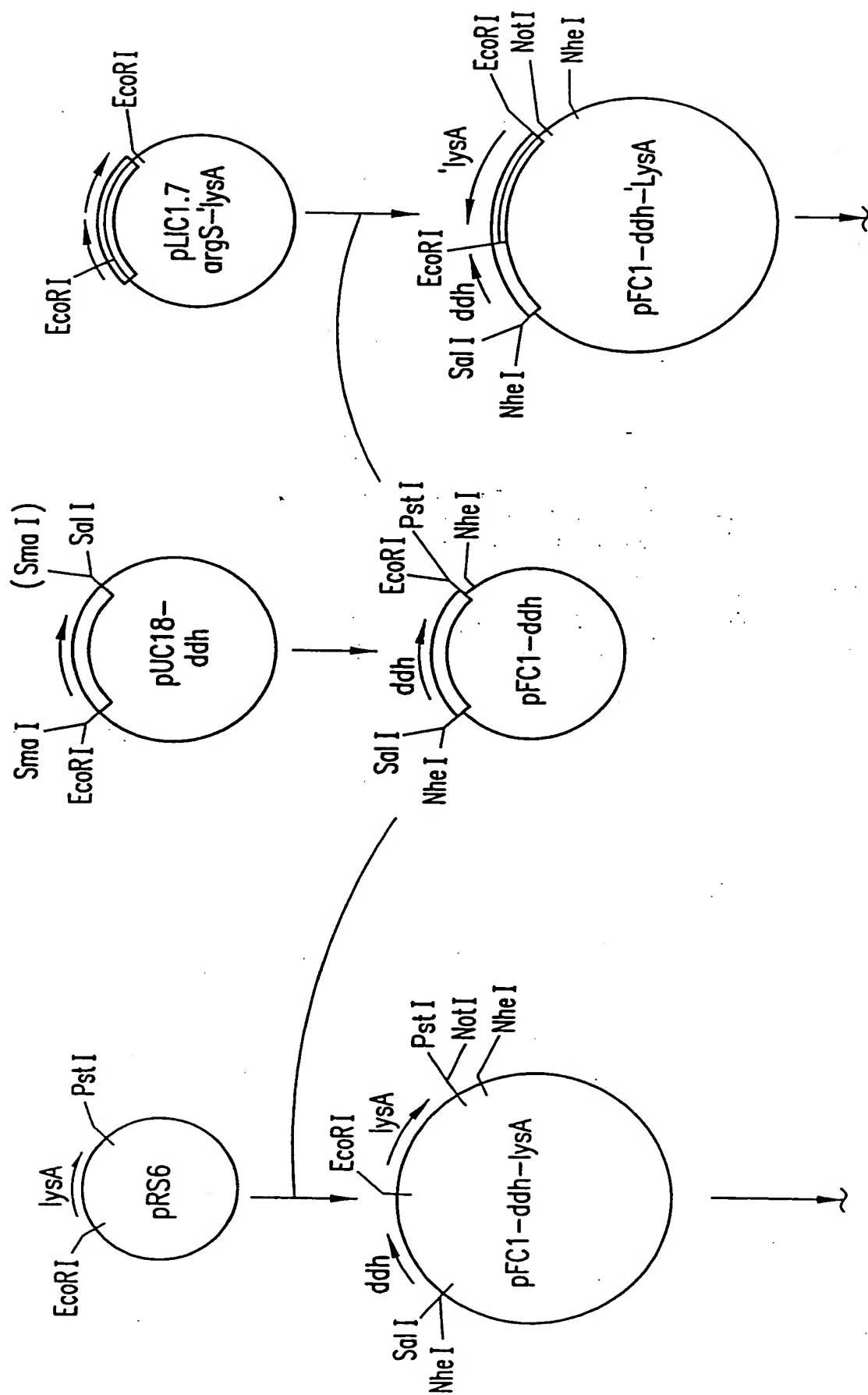


FIG.18A

CONT. ON FIG.18B

CONT. ON FIG.18B

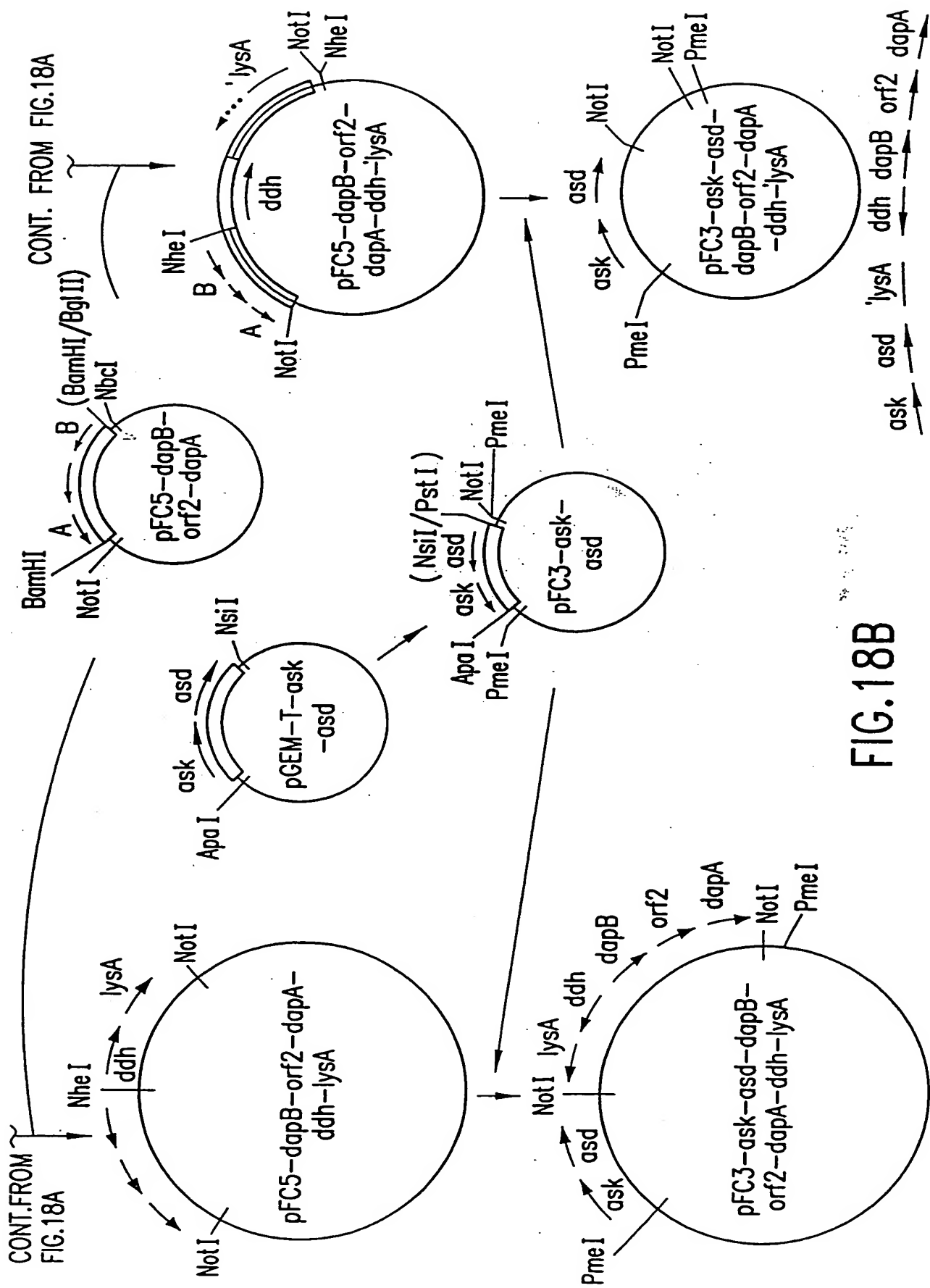


FIG. 18B

ATCC 13032	1		50
N13			
ATCC 21529			
Consensus	MALVVQKYGG	SSLESAERIR NVAERIVATK KAGNDVVVVC	SAMGDTTDEL
ATCC 13032	51		100
N13			
ATCC 21529			
Consensus	LELAAAVNPV	PPAREMDMLL TAGERISNAL VAMAIESLGA	EAQSFTGSQA
ATCC 13032	101		150
N13			
ATCC 21529			
Consensus	GVLTTTHERGN	ARIVDVTGPR VREALDEGKI CIVAGFQGVN	KETRDVTTLG
ATCC 13032	151		200
N13			
ATCC 21529			
Consensus	RGGSDTTAVA	LAAALNADVC EIYSDVDGVY TADPRIVPNA	QKLEKLSFEE
ATCC 13032	201		250
N13			
ATCC 21529			
Consensus	MLELAAVGSK	ILVLRVSVEYA RAFNVPLRVR SSYSNDPGTL	IAGSMEDIPV
ATCC 13032	251		300
N13			
ATCC 21529			
Consensus	EEAVLTGVAT	DKSEAKVTVL GISDKPGEAA KVFRALADAE	INIDMVLQNV
ATCC 13032	301		350
N13			
ATCC 21529			
Consensus	SSVEDGTTDI	TFTCPRADGR RAMEILKKLQ VQGNWTVLY	DDQVGKVS LV
ATCC 13032	351		400
N13			
ATCC 21529			
Consensus	GAGMKSHPGV	TAEFMEALRD VNVNIELIST SEIRISVLIR	EDDLAAARA
ATCC 13032	401	421	
N13			
ATCC 21529			
Consensus	LHEQFQLGGE	DEAVVYAGTG	R

FIG.19

HpaI-PvuII fragment comprising the P1 promoter (SEQ ID NO:17)

AACCGGTGTGGAGCCGACCATTCGCGAGGGCTGCACTGCAACGAGGTCGTAGTTTTGGTACATGGCTTCTG
GCCAGTTCATGGATTGGCTGCCGAAGAAGCTATAGGCATCGCCACCAGGGCCACCGGAGTTACCGAAGATG
GTGCCGTGCTTTTCGCCTTGGGCAGGGACCTTGACAAAGCCCACGCTGATATCGCCAAGTGAGGGATCAGA
ATAGTGCAATGGGCACGTCGATGCTGCCACATTGAGCGGAGGCAATATCTACCTGAGGTGGGCATTCTTCCC
AGCGGATGTTTTCTTGCGCTGCTGCAGTGGGCATTGATACCAAAAAGGGGCTAAGCGCAGTCGAGGCGGCA
AGAACTGCTACTACCTTTTTTATTGTCGAACGGGGCATTACGGCTCCAAGGACGTTTGTTTTCTGGGTCAG
TTACCCCAAAAAGCATATACAGAGACCAATGATTTTTTCATTAAAAAGGCAGGGATTTGTTATAAGTATGGG
TCGTATTCTGTGCGACGGGTGTACCTCGGCTAGAATTTCTCCCATGACACCAG

FIG. 20

MAKING pFC1-ddh P1lysA

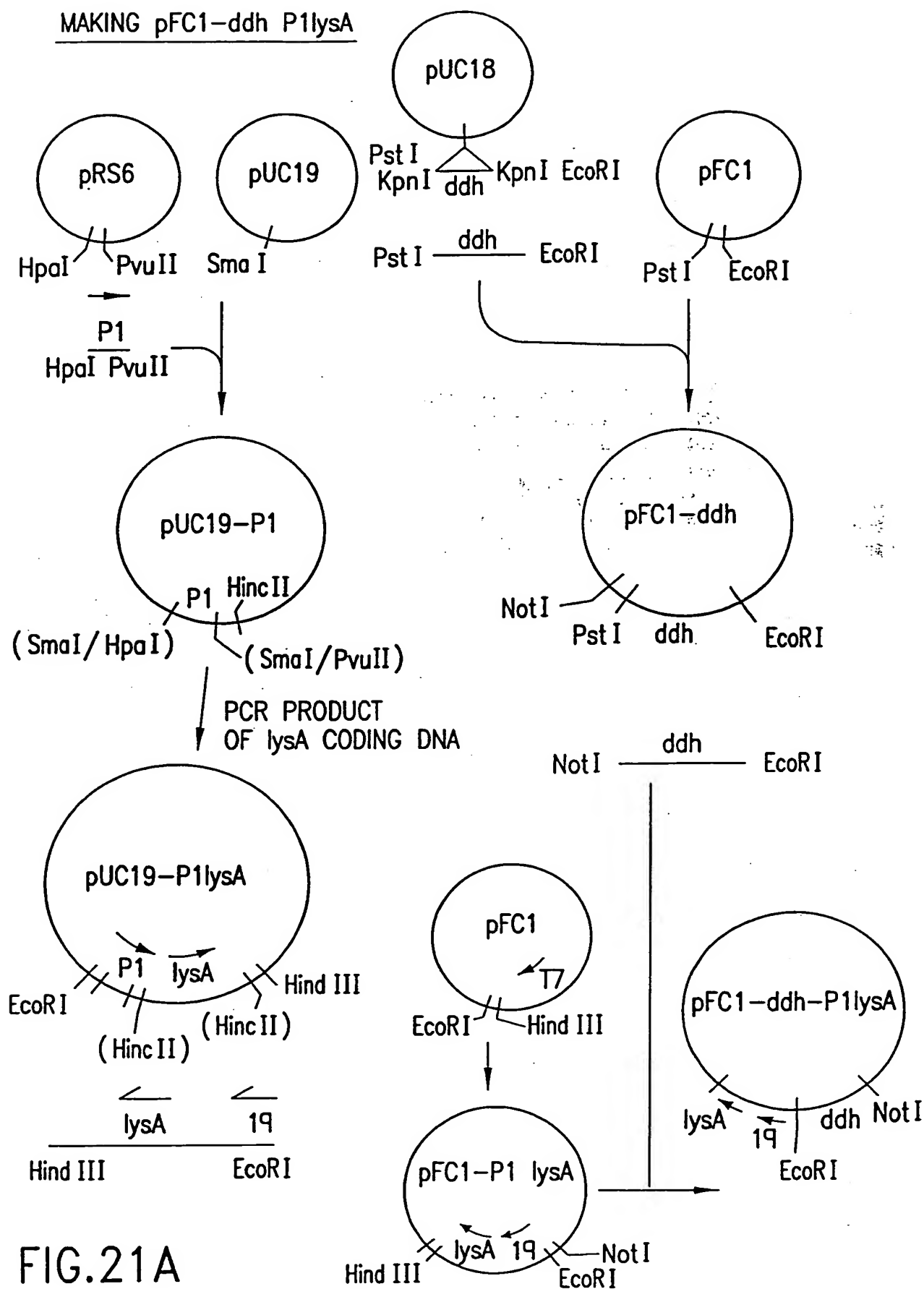


FIG.21A

MAKING pDElia2-KDABHP1L

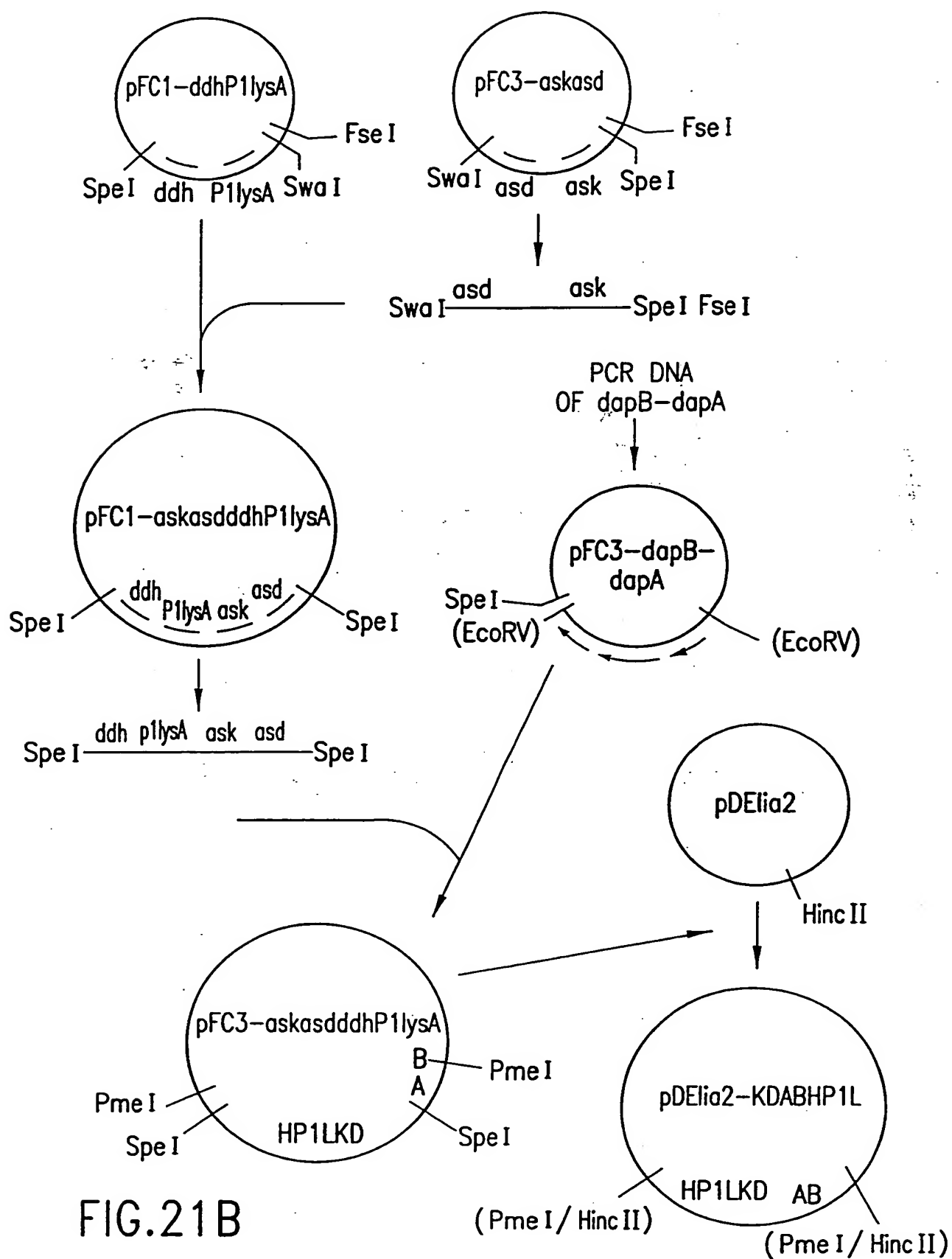


FIG.21B

MAKING pDElia2FC5-KDBHL

(FROM FIG.18A)

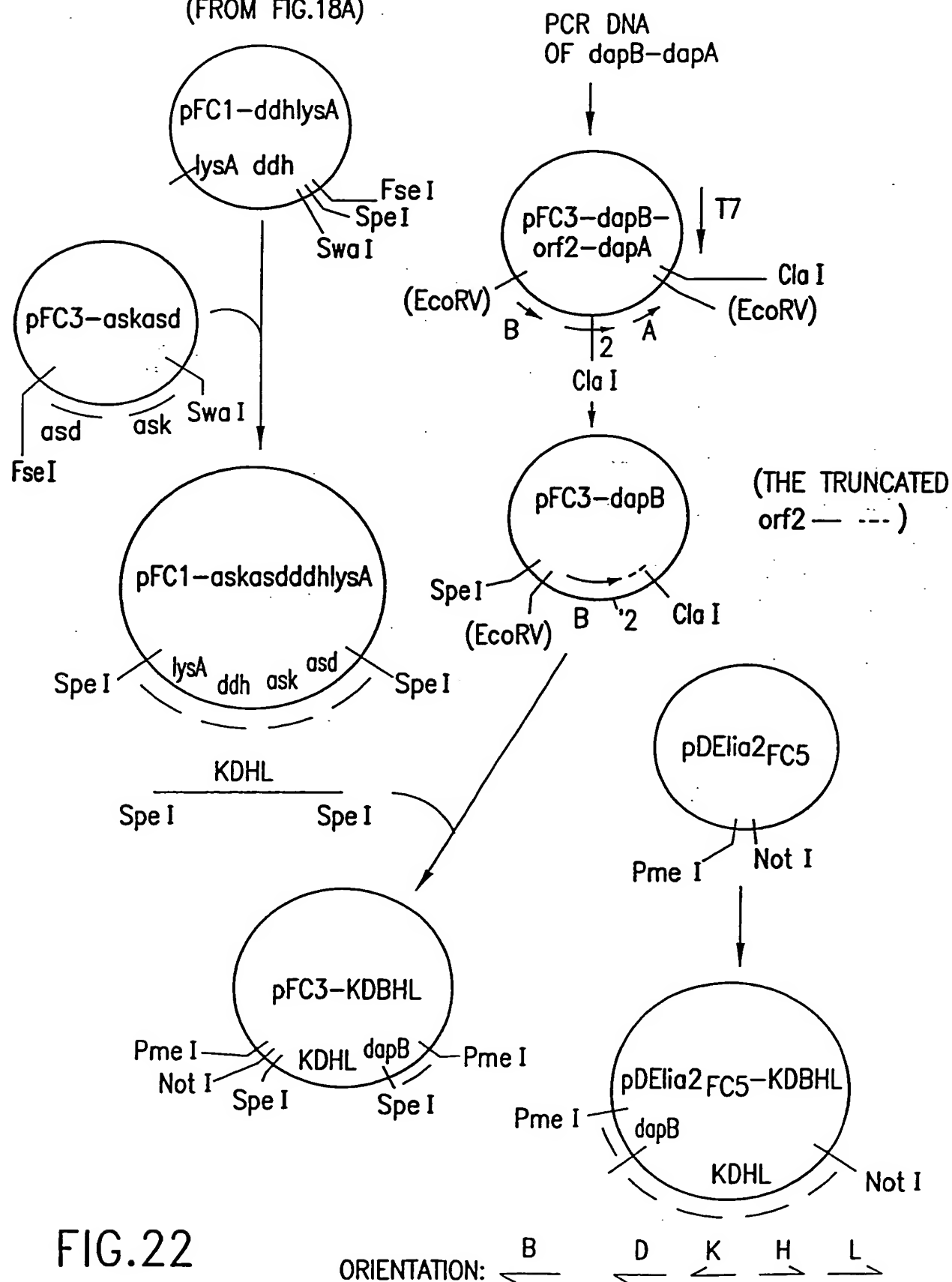


FIG.22

Nucleotide sequence of truncated ORF2 (SEQ ID NO:18)

```
1  GTGGCCGAAC AAGTTAAATT GAGCGTGGAG TTGATAGCGT GCAGTTCTTT
51  TACTCCACCC GCTGATGTTG AGTGGTCAAC TGATGTTGAG GGCGCGGAAG
101 CACTCGTCGA GTTTGCGGGT CGTGCCTGCT ACGAACTTT TGATAAGCCG
151 AACCCTCGAA CTGCTTCCAA TGCTGCGTAT CTGCGCCACA TCATGGAAGT
201 GGGGCACACT GCTTTGCTTG AGCATGCCAA TGCCACGATG TATATCCGAG
251 GCATTTCTCG GTCCGCGACC CATGAATTGG TCCGACACCG CCATTTTCC
301 TTCTCTCAAC TGTCTCAGCG TTTCGTGCAC AGCGGAGAAT CGGAAGTAGT
351 GGTGCCCACT CTCAT
```

FIG. 23

Truncated ORF2 amino acid sequence (SEQ ID NO:19)

GTGGCCGAACAAGTTAAATTGAGCGTGGAGTTGATAGCGTGCAGTTCTTTTACTCCACCC
1 -----+-----+-----+-----+-----+-----+ 60
M A E Q V K L S V E L I A C S S F T P P
GCTGATGTTGAGTGGTCAACTGATGTTGAGGGCGCGGAAGCACTCGTCGAGTTTGCGGGT
61 -----+-----+-----+-----+-----+-----+ 120
A D V E W S T D V E G A E A L V E F A G
CGTGCCTGCTACGAACTTTTGATAAGCCGAACCCTCGAACTGCTTCCAATGCTGCGTAT
121 -----+-----+-----+-----+-----+-----+ 180
R A C Y E T F D K P N P R T A S N A A Y
CTGCGCCACATCATGGAAGTGGGGCACACTGCTTTGCTTGAGCATGCCAATGCCACGATG
181 -----+-----+-----+-----+-----+-----+ 240
L R H I M E V G H T A L L E H A N A T M
TATATCCGAGGCATTTCTCGGTCCGCGACCCATGAATTGGTCCGACACCGCCATTTTCC
241 -----+-----+-----+-----+-----+-----+ 300
Y I R G I S R S A T H E L V R H R H F S
TTCTCTCAACTGTCTCAGCGTTTCGTGCACAGCGGAGAATCGGAAGTAGTGGTGCCCACT
301 -----+-----+-----+-----+-----+-----+ 360
F S Q L S Q R F V H S G E S E V V V P T
CTCAT ...
361 -----
L (I)

FIG. 24

Sequence of truncated LysA ('LysA) (NRRL-B11474) (SEQ ID NO:20)

ATGGCTACAGTTGAAAATTTCAATGAACTTCCCGCACACGTATGGCCACGCAATGCAGTG
CGCCAAGAAGACGGCGTTGTCACCGTCGCTGGTGTGCCTCTGCCTGACCTCGCTGAAGAA
TACGGAACCCCACTGTTTCGTAGTCGACGAGGACGATTTCCGTTCCCGCTGTCGCGACATG
GCTACCGCATTTCGGTGGACCAGGCAATGTGCACTACGCATCCAAAGCGTTCCTGACCAAG
ACCATTGCACGTTGGGTTGATGAAGAGGGGCTGGCACTGGACATTGCGTCCATCAATGAA
CTGGGCATTGCCCTGGCCGCTGGTTTCCCGGCCAGCCGTATCACCGCGCACGGCAACAAC
AAAGGCGTAGAGTTCCTGCGCGCGTTGGTTCAAACGGTGTGCGGCATGTGGTGCTGGAC
TCCGCGCAGGAATTGGAAGTGGTGGATTACGTTGCCGCTGGTGAAGGCAAGATCCAGGAC
GTGTTGATCCGCGTGAAGCCAGGTATCGAAGCCCACACCCACGAGTTCATCGCCACTAGC
CACGAAGACCAGAAGTTCGGATTCTCCCTGGCATCCGGTTCGCGATTCTGAAGCAGCGAAA
GCAGCCAACAATGCAGAGAACTTGAACCTGGTTGGTCTGCACTGCCATGTTGGTTCCAG
GTGTTGACGCCGAAGGCTTCAAGCTGGCAGCAGAGCGCGTGTGGGCCTGTACTCACAG
ATCCACAGCGAACTAGGTGTCGCCCTTCCTGAGCTGGACCTCGGTGGCGGATACGGCATC
GCCTACACTGCAGATGAGGAACCACTCAACGTCGCAGAAAGTCGCCTCCGACCT

FIG. 25

Truncated sequence of LysA (NRRL-B11474)

DIAMINOPIMELATE DECARBOXYLASE (LysA) (SEQ ID NO:21)

MATVENFNELPAHVWPRNAVRQEDGVVTVAGVPLPDLAEEYGTPLFVVDEDDFRSRCRDM
ATAFGGPGNVHYASKAFLTKTIARWVDEEGLALDIASINELGIALAAGFPASRITAHGNN
KGVEFLRALVQNGVGHVVLDSAQELELLDYVAAGEGKIQDVLIRVKPGIEAHTHEFIATS
HEDQKFGFSLASGSAFEAAKAANNAENLNLVGLHCHVGSQVFDÄEGFKLAAERVLGLYSQ
IHSELGVALPELDLGGGYGIAYTADDEEPLNVAEVASDL

FIG. 26